

[illegible]

Li et al.

Art Unit: 1646

Examiner: Basi, N.

Atty. Docket: 1488.1220000/EKS/EJH

Sir:

1. I, Steven M. Ruben, hereby declare and state as follows:

2. I am a named inventor of the captioned application, which is assigned to Human Genome Sciences, Inc. (HGS), and I am presently employed by HGS. The work described below was done by myself, under my supervision, or as part of a collaborative research effort with other individuals at HGS.

Human Epstein Barr Virus-Induced G-Protein Coupled Receptor-2 (EBI-2)

3. We obtained a cDNA clone encoding a human Epstein Barr virus-induced G-protein coupled receptor-2 (EBI-2) by screening a human hippocampus cDNA library. This clone was designated HHPGS02. We determined nucleotide sequence information for the HHPGS02 clone, as described below, using sequencing methods which were routine and publicly available as of the May 7, 1997 filing date of the present application. The HHPGS02 clone that we obtained this sequence information from was deposited with the American Type Culture

Collection (ATCC) on April 28, 1997 and was given ATCC Accession No. 209003. (See Attachment A.)

4. Evidence that the human HHPGS02 cDNA was deposited at the ATCC as Accession No. 209003 is provided by comparing the ATCC Deposit Receipt (Attachment A) with the information provided in the IRIS notebook page (entitled "Sequence Worksheet") included herewith as the first page of Attachment B.¹ The section of the page entitled "Sequence Information" corresponds clone HHPGS02² with the "HGS Code," 405439. HGS Code 405439 represents a particular sequence entry in IRIS for cDNA clone HHPGS02. HGS Code 405439 appears as the identifier on the ATCC deposit receipt. (See Attachment A.) This indicates that the clone used to obtain the sequence information of HGS Code 405439 was deposited. In other words, even though, as explained below, SEQ ID NO:1 and SEQ ID NO:2 in the Sequence Listing of the present application as originally filed, had typographical errors due to attorney error, the human HHPGS02 cDNA clone used to obtain the original, correct sequence data was deposited at the ATCC.

5. Attachment B provides four pages of data from the IRIS electronic notebook which shows the sequencing results of the human EBI-2 cDNA clone (*i.e.*, HHPGS02). The HHPGS02 sequence was obtained using a 373 Automated DNA sequencer (Applied Biosystems, Inc.). Sequencing accuracy using this method is predicted to be greater than 97%.

6. The information obtained from the HHPGS02 sequencing run differs from the Sequence Listing currently on file in the present application at four positions. In particular, SEQ

¹IRIS is an electronic notebook used by HGS scientists to enter and maintain sequence data.

²The "XX" designation added to the 7-character clone ID on the IRIS Notebook pages, e.g., HHPGS02, merely indicates that the sequence of that clone is full-length.

ID NO:1 contains typographical errors at the following nucleotide positions: position 242, which should be A rather than T; position 266, which should be C rather than A; position 1870 (in the 3' untranslated region), where a T should be deleted, and position 2206, where an N should be deleted. These typographical errors in the nucleotide sequence result in the following errors to the encoded amino acid sequence depicted as SEQ IDNO:2: an isoleucine at position 6 should be replaced with an asparagine, and an asparagine at position 14 should be replaced with a threonine. Both of these changes are reflected in the HHPGS02 amino acid sequence data shown on the third and fourth pages of Attachment B, as well as in an amino acid alignment originally filed with the present application as Figure 2.

7. I believe that the actual nucleotide sequence of the human HHPGS02 cDNA clone is the same as that originally entered in the IRIS notebook.

8. I am of the opinion that the correct EBI-2 nucleotide and amino acid sequences would have been apparent to one skilled in the art in possession of ATCC Deposit No. 209003 and the data from the HHPGS02 sequencing run, as of the May 7, 1997 filing date of the present application. This is so because the correct EBI-2 coding sequence can be readily determined from the deposited clone and methods for sequencing this clone were routine in the art in May of 1997.

Human Endothelium Differentiation Gene-1-Like (EDG-1-Like) G-Protein Coupled Receptor

9. We obtained a cDNA clone encoding a human endothelium differentiation gene-1-like (EDG-1-like) G-protein coupled receptor by screening a cDNA library derived from human activated neutrophils. This clone was designated HNF DL69. We determined nucleotide sequence information for the HNF DL69 clone, as described below, using sequencing methods which were routine and publicly available as of the May 7, 1997 filing date of the present application. The

HNFDL69 clone that we obtained this sequence information from was deposited with the American Type Culture Collection (ATCC) on April 28, 1997 and was given ATCC Accession No. 209004 (*See Attachment A.*)

10. Evidence that the human HNFDL69 cDNA was deposited at the ATCC as Accession No. 209004 is provided by comparing the ATCC Deposit Receipt (Attachment A) with the information provided in the IRIS notebook page (entitled "Sequence Worksheet") included herewith as the first page of Attachment C. The section of the page entitled "Sequence Information" corresponds clone HNFDL69 with the "HGS Code" 563238. HGS Code 563238, represents a particular sequence entry in IRIS for cDNA clone, HNFDL69. HGS code 563238 appears as the identifier on the ATCC deposit receipt. (*See Attachment A.*) This indicates that the clone used to obtain the sequence information of HGS Code 563238 was deposited. In other words, even though, as explained below, SEQ ID NO:3 and SEQ ID NO:4 of the Sequence Listing in the present application as originally filed, had typographical errors due to attorney error, the human HNFDL69 cDNA clone used to obtain the original, correct sequence data was deposited at the ATCC.

11. Attachment C provides three pages of data from the IRIS electronic notebook which shows the sequencing results of the human EDG-1-like cDNA clone (*i.e.*, HNFDL69). The HNFDL69 sequence was obtained using a 373 Automated DNA sequencer (Applied Biosystems, Inc.). Sequencing accuracy using this method is predicted to be greater than 97%.

12. The information obtained from the HNFDL69 nucleotide sequencing run differs from the Sequence Listing currently on file in the present application in two positions. In particular, SEQ ID NO:3 contains typographical errors at the following nucleotide positions: position 828, which should be T rather than C; and position 831, which should be T rather than

A. Note that this latter typographical error introduced a stop codon into the open reading frame, causing the amino acid sequence, as translated from the sequence with the typographical error, to stop at position 260. Accordingly, these typographical errors in the nucleotide sequence result in the following errors to the encoded amino acid sequence depicted as SEQ IDNO:4: the serine at position 260 should be replaced with phenylalanine, and the translation should continue to amino acid 384, as depicted in the original translation provided on the third page of Attachment

C. SEQ ID NO:4 further contains typographical errors at the following amino acid positions: position 191, which should be Asp rather than Asn, position 202, which should be Lys rather than Arg, and position 204, which should be Tyr rather than Thr. In addition, the translation should start with the Met at position 1, rather than the Ala at position -16. Both of the nucleotide sequence changes are reflected in the HNFDL69 nucleotide sequence data shown on the first and second pages of Attachment C, and the amino acid sequence changes are reflected in the HNFDL69 amino acid sequence data shown on the third page of Attachment C. In addition, The amino acid sequence data is reflected in an amino acid alignment originally filed with the present application as Figure 4, except for five residues at the 3' end of the polypeptide. These latter five residues are not in the alignment simply because they did not align with the second sequence in Figure 4, i.e., SEQ ID NO:18.

13. I believe that the actual nucleotide sequence of the human HNFDL69 cDNA clone is the same as that originally entered in the IRIS notebook.

14. I am of the opinion that the correct EDG-1-like nucleotide and amino acid sequences would have been apparent to one skilled in the art in possession of ATCC Deposit No. 209004 and the data from the HNF DL69 sequencing run, as of the May 7, 1997 filing date of the present application. This is so because the correct EDG-1-like coding sequence can be readily

$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$

2/15/99

Alan T. Miller

Steven M. Ruben



American Type Culture Collection

12301 Parklawn Drive • Rockville, MD 20852 USA • Telephone: 301-231-5519 or 231-5532 • FAX: 301-816-4366

BUDAPEST TREATY ON THE INTERNATIONAL RECOGNITION OF
THE DEPOSIT OF MICROORGANISMS FOR THE PURPOSES OF PATENT PROCEDURE

INTERNATIONAL FORM

RECEIPT IN THE CASE OF AN ORIGINAL DEPOSIT ISSUED PURSUANT TO RULE 7.3
AND VIABILITY STATEMENT ISSUED PURSUANT TO RULE 10.2

RECEIVED

To: (Name and Address of Depositor or Attorney)

Human Genome Sciences, Inc.
Attn: Robert H. Benson
9410 Key West Avenue
Rockville, MD 20850

HGS PATENT DEPT.

351A1-SKB

Deposited on Behalf of: Human Genome Sciences, Inc. (Ref. PF351PP-SKB)

PF351PP-SKB

Identification Reference by Depositor:

ATCC Designation

DNA Plasmid 405439
DNA Plasmid 563238

209003 ✓
209004 ✓

The deposits were accompanied by: ___ a scientific description ___ a proposed taxonomic description indicated above.

The deposits were received by this International Depository Authority and have been accepted.

AT YOUR REQUEST:

☒ We will inform you of requests for the strains for 30 years.

The strains will be made available if a patent office signatory to the Budapest Treaty certifies one's right to receive, or if a U.S. Patent is issued citing the strains, and ATCC is instructed by the United States Patent & Trademark Office or the depositor to release said strains.

If the cultures should die or be destroyed during the effective term of the deposit, it shall be your responsibility to replace them with living cultures of the same.

The strains will be maintained for a period of at least 30 years from date of deposit, or five years after the most recent request for a sample, whichever is longer. The United States and many other countries are signatory to the Budapest Treaty.

The viability of the cultures cited above was tested

On that date, the cultures were viable.

International Depository Authority: American Type Culture Collection, Rockville, Md. 20852 USA

Signature of person having authority to represent ATCC:

Barbara M. Hailey

Barbara M. Hailey, Administrator, Patent Depository

Date:



Human Genome Sciences, Inc.
Sequence Worksheet
HHPGS02XX: KIAA0001 [Homo sapiens]

Sequence Information

Gene Name: KIAA0001 [Homo sapiens]

HGS Code: 405439

Sequence ID: HHPGS02XX

Library Name: Human Hippocampus

Library Catalog: H0051

Date Sequenced:

Lab Sequenced: HGS

Group ID: 56754

Class: 2

Date Scored:

Lab Scored: HGS

In Group: 23

Previous Class: 2

Search Results

Overlap	Score	Description
gi 292057	136	EBI 2: EBV induced G-protein coupled receptor [Homo sapiens] >pir B45680 B45680 G protein-coupled peptide receptor EBI 2 -
gi 471121 gnl	169	angiotensin II type 1b receptor [Homo sapiens] >gi 471121 gnl PID d1003474 angiotensin II type 1b receptor [Homo sapiens] >
gi 2580588	273	(AF002986) platelet activating receptor homolog [Homo sapiens] >sp O14626 O14626 PLATELET ACTIVATING RECEPTOR HOMOLOG.
gi 2459585	528	VTR 15-20 receptor [Rattus norvegicus] >sp O35881 KI01_RAT PROBABLE G PROTEIN-COUPLED RECEPTOR VTR 15-20.
gi 285995	538	KIAA0001 [Homo sapiens] >sp Q15391 KI01_HUMAN PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.
gi 299615 gp	169	AT1 angiotensin II receptor [Oryctolagus sp.] >pir S A48857 AT1 angiotensin II receptor, AT1 ANG II receptor - rabbit >sp P
gi 217670 gp	171	angiotensin II receptor [Sus sp.] >gi 217670 gp D11340 PIGA2R_1 angiotensin II receptor [Sus sp.] >sp P30555 AG2R_PIG TYPE-
gi 44 gp K62	171	adrenal angiotensin II type-1 receptor [Bos taurus] >pir S S15403 angiotensin II receptor type 1 - bovine >sp P25104 AG2R_B
gi 292057 gp	159	EBI 2: EBV induced G-protein coupled receptor [Homo sapiens] >pir S B45680 G protein-coupled peptide receptor=EBI 2 - human
gi 285995 gp	686	ORF [Homo sapiens] >gi 285995 gp D13626 HUMRSC338_1 ORF [Homo sapiens]

Sequence

ID HHPGS02XX unannotated; DNA; 2247 BP.

KIAA0001 [Homo sapiens]

XX
XX
XX
XX

Sequence 2247 BP;

GCACGAGGAA CAGAACACTT TCTCATGTCC AGGTCAGAT TACAAAGCCA CTCACACTTT
TACTGACGAA AACTCAGGAA AATCTTATTC ACAAGAGGT TTGGCACTTA AACTAAGACA
TTAAAGGAA AATACAGAT GCCACTTGC AGGTCGAAT AACTACTACT TACTGATAC
ATTCAAAACC TCCAGATCA ACAGTATCA GGTAACCAAC AAGAAATGCA AGCGTGCAC
AATCTCACT CTGGGCTTG GAACACAGT CTGTGACCA GAGACTACAA AATCAACCAG
GTCTCTTCC CACTGTCTA CACTGTCTG TTTTGTGTG GACTTATCAC AAATGGCTTG
CGATGAGGA TTTTCTTCA AATCCGAGT AATCAAACT TTATTATTIT TCTTAAGAAC



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Sequence Worksheet

HHPGS02XX: KIAA0001 [Homo sapiens]

ACAGTCATTT CTGATCTTCT CATTGATCTG ACTTTTCCAT TCAGAAATTCCT TAGTGATGCC
AAACTGGGAA CAGGACCACT GAGAACTTTT GGTGTGCAAG TTACTTCGGT CATATTTTAT
TTTCAATATG ATATTCAGTAT TTCAATTCTG GACTGATTA CTATCGATCG CTACAGAAG
ACGACCAAGC CATTTAAAC ATCCAACCC AAAATCTCT TGGGGCTTA GATTCCTCT
GTTCATCT GGGCATTCAT GTTCTTACTC TCTTGGCTA ACATGATTCCT GACCAACAG
CAGCCGAGAG ACAAGATGT GAGAAATCC TCTTTCCCTA AATCAGAGTT CGGTCTAGTC
TGCGATGAAG TAGTAAATTA CATCTGTCAA GTCATTTTCT GGATTAATTT CTAAATGTT
ATTGTATGTT ATCACTCAT TACAAGAGAA CTGACCGGT CATACGTAAG AACGAGGGT
GTAGGTAAAG TCCCCAGGAA AAGGTGAAC GTCAAGTTT TCATTATCAT TCGTGTATTC
TTTATTTGTT TTGTTCCTTT CCATTTTGCC CGAATTCCTT ACACCTGAG CCNAAACCCG
GATGTCCTTG ACTGCACtGC tGAAATTACT CIGTCTAAG TGAAGAGAG CACTCTGTG
TTAACTTTCCT TTAATGCATG CCTGATCCG TTCACTAAT TTTTCCCTTG CAAGTCCTC
AGAAATTCCT TGATTAAGTAT GCTGAAGTC OCCAATCTG CAACATCTCT GTCCAGAGAC
AATAGGAAA AAGACAGGA TGGTGTGAC CCAATGAAG AGACTCCAAT GTAAACAAAT
TAACTAAGA AATATTTCAA TCTCTTTG TGTCAGAACTC GTTAAGCAA AGGCTAAGT
AAAATATTA ACTGACGAG AAGCACTTAA GTTAATATA ATGACTTAA AGAACAGAA
GATTACAAAA GCAATTTTCA TTATCTTTC CAGTATGAAG AGCTATCTTA AAATATAGAA
AACTAATCTA AACTGTAGCT GTATTAGCAG CAAACAAAC GACATCCAAT TGTCAATGCTG
CATGCAAAAC TACACAGAAAT TCATGTTTG GCAGAGTTT GGCATAAATGA GTAATCATAT
AATATTTACT GTATTTTAA AAATACATTA TCGTTCAAA TTTTATTTT TCATTAATCAA
CTAAGAAGA AGCATCAAT GGAATTAATC TTCTTAACAA AAATGATAGT TAAATGTAT
ATATATCTA GTCCCTTAAC CAATCTGA CTATTTGGGA TACTTATTA AATTTAAGTA
AGTGGATAC ACAAGAATA ATAACTATA ACTTTTCAAT ATTAGCCAAA AACCTAAGG
ATTTAAACTA ATTGAACCTG TATTGATG GACTTAATTT TTTATGTTA TTTAGAAGAT
AAAGATTAA GAGACCTTT ACAATTAAGA GAGAAATAT CGAAGTCATT AAAATTAAGA
GACTTACTTT TATGACATTC TAACTAATA AAATATAGAA ATATTTCTT AATCTAGAG
AACTATGTT TACTAATTTT TTACAACCTC AATTAATACA TCACGACAC TTACCTTTAT
TAAATAGCTT CTAGAAAAATA GCTGCTAAT AGGTTAATGA ACATTTTAC TTAGTGAAGA
AAATTTAAT AAATATGATT ACAAGGTGC ACAGCATAC TACTGAGAG AAGTGAATG
ATCTGTTGT AATTACTTGT TTGTATGCT GTGTATTAATA TACAATTTTA CATTAACCTC
TAAAtcatta aaaaaaaaaa aaaaaa

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Sequence Notes

Sequence Information

Gene Name: KIAA0001 [Homo sapiens] HGS Code: 405439 Sequence ID: HHPGS02XX
Library Name: Human Hippocampus Library Catalog: H0051
Date Sequenced: Lab Sequenced: HGS Group ID: 56754 Class: 2
Date Scored: Lab Scored: HGS In Group: 23 Previous Class: 2

Search Results

Overlap	Score	Description
gi 292057	136	EBI 2: EBV induced G-protein coupled receptor [Homo sapiens] >pir B45680 B45680 G protein-coupled peptide receptor EBI 2 -
gi 471121 gm	169	angiotensin II type 1b receptor [Homo sapiens] >gi 471121 gm PID d1003474 angiotensin II type 1b receptor [Homo sapiens] >
gi 2580588	273	(AF002986) platelet activating receptor homolog [Homo sapiens] >sp O14626 O14626 PLATELET ACTIVATING RECEPTOR HOMOLOG.
gi 2459585	528	VTR 15-20 receptor [Rattus norvegicus] >sp 035881 KI01_RAT PROBABLE G PROTEIN-COUPLED RECEPTOR VTR 15-20.
gi 285995	538	KIAA0001 [Homo sapiens] >sp Q15391 KI01_HUMAN PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.
gi 299615 gp	169	AT1 angiotensin II receptor [Oryctolagus sp.] >pir S A48857 AT1 angiotensin II receptor, AT1 ANG II receptor - rabbit >sp P
gi 217670 gp	171	angiotensin II receptor [Sus sp.] >gi 217670 gp D11340 PIGA2R_1 angiotensin II receptor [Sus sp.] >sp P30555 AG2R_PIG TYPE-
gi 4419p X62	171	adrenal angiotensin II type-1 receptor [Bos taurus] >pir S S15403 angiotensin II receptor type 1 - bovine >sp P25104 AG2R_B
gi 292057 gp	159	EBI 2: EBV induced G-protein coupled receptor [Homo sapiens] >pir S B45680 G protein-coupled peptide receptor=EBI 2 - human,
gi 285995 gp	686	ORF [Homo sapiens] >gi 285995 gp D13626 HUMSC338_1 ORF [Homo sapiens]

Sequence

ID HHPGS02XX unannotated; DNA; 749 BP.
KIAA0001 [Homo sapiens]

Sequence 749 BP:
ARGTEHFTMS RVRLQEHSL Y*RLKRSSI TKRGN*TKT LKGGYQMPIC RLQ*LLITGY
IQLQNGQLS GNGQEMQAVD NLTSAPGNTS LCTRDYKITQ VLEPILYTVL FFGELITNKL
AMRLIEQURS KSNFTIEFLKN TVISDLIMTL TTFPKILSDA KLGTGPIRPF VCQVTSVIFY
FTMTSISFL GLTTIDRYOK TTRPEKTSNP KNLGAKILS VWIWMFELL SLPMWILINR
QPRDKNVKCC SFLKSEFGLV WHEIVANYIQ VIFMINFELIV IVCYTLITKE IYRSYVTRTG
VGVKPRKKVN VKVFTIIAVF FICEVPEHFA RLPYTLSQTR DVFDCIAENT LEYVKESTLW
LFTLNACLDP FIFYFLCKSF RNSLISMLKC FNSATSLSQD NRKKEQDGD PNEETPM*TN



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Sequence Worksheet
HHPGS02XX: KIAA0001 [Homo sapiens]

*LRKYNLFV FRTR*SKALS KNIN*RRSN* VNNDSKETE DYKSNEHLPF QYEKL S*NIE
N*SKL*LY*Q QNKRHPIVML HAKLHRILHL AEFWQNE*SY NITYCNF*NIL SPTTILFFHNQ
LRNDQOLDIT FLEPMIVKMY TYPSPILTKS* PIGILIKI*V SGHKE**IL TFHY*PKT*G
I*TN*NCI*L DLIFYVYLED KDLRRPLQ*R EESISKIK*G DLL*HSNIR KYRNTSLIE
KLVLLIFYNE NNTTDTYLY *LASRK*LLI RLMNLLP**K KIN*I*LOSC TA*LLRCK*L
ICL*LLWCIG VKIQIYIKL *ILKKKKK

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Sequence Notes



Human Genome Sciences, Inc. Sequence Worksheet

HNFDL69XX: H.sapiens repeat polymorphism in LIPE gene for hor

Sequence Information

Gene Name: H.sapiens repeat polymorphism in LIPE gene 1 HGS Code: 563238 Sequence ID: HNFDL69XX
Library Name: Human Neutrophil, Activated Library Catalog: H0271
Date Sequenced: Lab Sequenced: HGS Group ID: 2514675 Class: 1
Date Scored: Lab Scored: HGS In Group: 18 Previous Class: 1

Search Results

Overlap	Score	Description
gb X65642 1	260	H.sapiens repeat polymorphism in LIPE gene for hormone sensitive lipase.
gp X54937 HS	93	cannabinoid receptor [Homo sapiens] >pir S S17595 cannabinoid receptor - human >sp P21554 CB1R_HUMAN CANNABINOID RECEPTOR 1
gp X55812 RM	93	putative cannabinoid receptor [Rattus norvegicus] >pir S A33117 cannabinoid receptor - rat >sp P20272 CB1R_RAT CANNABINOID 1
gp L20334 MC	141	EDG-like receptor [Mus musculus]
gp U10699 RM	152	pH218 [Rattus norvegicus] >pir S J01465 probable G protein-coupled receptor - rat
gp M31210 HUI	210	BOGF1 gene product [Homo sapiens] >pir S A35300 G protein-coupled receptor edg-1 - human >sp P21453 EDG1_HUMAN PROBABLE G P

Sequence

ID HNFDL69XX unannotated; DNA; 1637 BP.
DE H.sapiens repeat polymorphism in LIPE gene for hormone sensitive lipase.
XX
DT

Sequence 1637 BP;
GCCACGAGCC CACCTTGGT CGGCTTACG TCAGCTTTGG GGGAGGCCA TGAACGCCAC
GGGAGCTTTG GTGGCTTTGG AGTCTTGGCA ACAGCTGGCG GCGGCGGGC ACAGCGGGCT
CATTTGTTCTG CACTTACACC ACTTGGGGCG GCTGGCGGGC CGCGGGGGC CGAGGATGG
CGGCTTGGCG GCGCTTGGCG GCTTGTGGT GCGGCGGAC TGCCTTGGTG TGCTTGAGAA
CTTCTTGGTG CTGGCGGCA TCACGAGCCA CATTGGGTG CAAGCTGGG TCTTACTATTG
CCTTGTGAC ATTACGATGA GTTACCTTCT CAGCGGGCG GCTTACCTTG CCAACGTGCT
GCTGTGGGG GCGCGACCT TCCGTCTGG GCGGCGGCG TGGTTCCTAC GGAAGGGGCT
GCTTCTTACC GCGCTTGGCG CTTCCACCTT CAGCTTGGCT TTCCTTGGAG GGTTCGGCTT
TGCCACCATG GTGGCGGGCG TGCGGAGAG CGGGGCCACC AAGACGAGC GCGTCTAAGG
CTTCAATGCG CTCTCTGGC TGTGGCGCG GCTTCTGGCG ATGCTTGGCTT TGCTTGGGCTG



HGS

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Sequence Worksheet

HNFDL69XX: H.sapiens repeat polymorphism in LIPE gene for hor

GAACTGCTTG TGCGCTTTG AOCCTGCTC CAGCTTCTG CCCCTTACT CCAAGCCTA
CATCTCTTC TGCTTGTA TCTTGCCCG GCTCTGCCC ACCATCATG GCTCTATGG
GGCATCTTC GCGCTGTGC AGGCAGCCG GCAGAGGCC CCAAGCCAG CGGCCCGCG
CAAGCCCGC GCGCTGTGA AGACGGTGT GATGATCTG CAGCCCTCT TGGTGTCTG
GGACCACTC TTGCGGCTG TGCTTGCCG GCTCTTGGC TCCAACTCT GGGCCAGGA
GTACTGCGG GCATGACT GATCTTGGC CCTGCGCTC CTCAACTCG CGGTCAACC
CATCATCTAC TCTTGCCGA GCAGGAGGT GTGAGAGCC GTGCTCAGT TCTCTGCTG
CGGTGTCTC GCGCTGCGA TGCGAGGCC CGGGACTGC CTGCTCAGT TCTCTGCTG
TCACTCCGA GCTTCCACA CCGACAGCT TCTGAGGCC AGGACAGCT TTGCGGCTC
CGCTGCTC AGCTTTCGA TGCGGAGCC CCTGTCCAG ATCTCCAGG TGCGAGCAT
CTGAAGTTC AGCTTTCGT GTGATGTGT CAACCAACG GTGCTGCCA GGCAGGCCCT
CCTGGGTAC AGGAGCTGT GTGACGCAA CCTGCGCTG TATGGGAGC AGGGAACGG
ACAGCCCC ATGACTTGC CCGTGGCTT CTGCGGCTT CTGAGCCAT ATGACTTGC
CCAATCCCTA TGCTCACCC TGACCAAGGA GGCACCAAC CCACCTCCC GTAGAGCAG
AGAGCAACCT GGTGTGGGG CGAGTGGGT CCCACAACC CGCTTCTGT GTGATCTGG
GGAAGTCCG GCGCTCTCT GGGCTCAGT AGGCTTCCA GGTGCAAGG GGTGACTGT
GGATGCAAT CCTGCGAAC ATTGAAGTT GATCATGTGA AAAAAAAAAA AAAAAAAAAA
AAAAAAAAA AAAAAAA

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Sequence Notes



HGS

Human Genome Sciences, Inc.
Sequence Worksheet
HNFDL69XX: H.sapiens repeat polymorphism in LIPE gene for hor

Sequence Information

Gene Name: H.sapiens repeat polymorphism in LIPE gene 1
Library Name: Human Neutrophil, Activated
Date Sequenced: Lab Sequenced: HGS
Date Scored: Lab Scored: HGS
HGS Code: 563238
Library Catalog: H0271
Sequence ID: HNFDL69XX
Group ID: 2514675
In Group: 18
Class: 1
Previous Class: 1

Search Results

Overlap	Score	Description
gb X65642	260	H.sapiens repeat polymorphism in LIPE gene for hormone sensitive lipase.
gp X54937 HS	93	cannabinoid receptor [Homo sapiens] >pir s S17595 cannabinoid receptor - human >sp P21554 CB1R_HUMAN CANNABINOID RECEPTOR 1
gp X55812 RN	93	putative cannabinoid receptor [Rattus norvegicus] >pir s A33117 cannabinoid receptor - rat >sp P20272 CB1R_RAT CANNABINOID 1
gp L20334 MC	141	EDG-like receptor [Mus musculus]
gp U10699 RN	152	ph218 [Rattus norvegicus] >pir s Jc1465 probable G protein-coupled receptor - rat
gp M31210 HU	210	BCGF1 gene product [Homo sapiens] >pir s A35300 G protein-coupled receptor edg-1 - human >sp P21453 EDG1_HUMAN PROBABLE G P

Sequence

ID HNFDL69XX unannotated; DNA; 545 BP.
DE H.sapiens repeat polymorphism in LIPE gene for hormone sensitive lipase.
XX
DT

Sequence 545 BP;
ARAHPASGLS QPRGEAMNAT GTFVAPESQO QLAAGHSRL IWLHYNHSGR LAGRGPEDEG
GLGALRGELSV AASCLVLEN LVLTAITSH MRSQRWVYYC LVNTTMSDL TGAAYLANVL
LSGARTFRLA PAQWFLRKL LFTALAASTF SLFTAGLARF ATMVRPAES GATKTSRVYG
FTGLCWLLAA LIGMLPLGW NCLCAFDRCs SLPLYSKRY ILFCLVTFAG VIATDMLYG
AIFRLVQASG QKAPRPAARR KARLLKTVL MLLAFLVOW GPLEGILLAD VFGSNLWAQE
YLKMDWLLA LAVINSAVNP ILYSRSREV CRAVLSTLOC GCIRLGMRGP EDCIARAVEA
HSGASTTDS LRPDSFRGS RSLSRMRER LSSISSVRSI *SCSLACGMC NHRVRARQAL
LGYRLCARN LALYGEQGTG QAPMDLPGEL SALTIPYELA HCLMLTLKE ATPPPRRSR
EHBGVASGF PTPRLDSG EVPAPIWASV GLPGCKGNTV GCMPOH*SS IMWKKKKKKK
KKKK



HGS

Human Genome Sciences, Inc.
Sequence Worksheet
HNF69XX: H.sapiens repeat polymorphism in LIPE gene for hor

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Sequence Notes